(1) GENERAL INFORMATION:

(i) APPLICANTS: Goodearl, Andrew; Stroobant, Paul; Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; Chen, Maio Su; Hiles, Ian

(ii) TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use

(iii) NUMBER OF SEQUENCES: 184

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(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
    (B) COMPUTER: IBM
    (C) OPERATING SYSTEM: PC-DOS
    (D) SOFTWARE: Wordperfect

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    (B) FILING DATE:
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    (A) APPLICATION NUMBER: 08/036,555
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    (A) APPLICATION NUMBER: 07/863,703
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(vii) PRIOR APPLICATION DATA:
              (A) APPLICATION NUMBER: U.K. 91 07566.3
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       (viii) ATTORNEY/AGENT INFORMATION:
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              (B) REGISTRATION NUMBER: 34,266
              (C) REFERENCE/DOCKET NUMBER: LUD 5250.18

         (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 8
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Lys Gly Asp Ala His Thr Glu
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 13
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (ix) FEATURE:
         (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                  Xaa in position 12 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 12
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear
   (ix) FEATURE:
       (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                        Xaa in position 10 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 9
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear
   (ix) FEATURE:
       (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 7
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear
   (ix) FEATURE:
       (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine
                                 and Xaa in position 12 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                 Xaa in position 8 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                 Xaa in position 7 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1   5   10   15

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 8 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 2 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
 1   5   10   15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
             20   25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2003
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear ·
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N in positions 31 and 32 could be either
                                  A or G.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:


```
GGAATTCCTT TTTTTTTTTT TTTTTTTCTT NNTTTTTTTT TGCCCTTATA CCTCTTCGCC      60
TTTCTGTGGT TCCATCCACT TCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT     120
GCACCCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG     180
CGAGGGGAAG GAAAAGGGAG GCAGCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC     240
AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC       291
                           Met Arg Trp Arg Arg Ala Pro Arg Arg
                            1               5
```

```
TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC      339
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg
 10               15                  20                      25
```

```
TCG TCG CCG CCG CTG CCG CTG CTG CCA CTA CTG CTG CTG CTG GGG ACC      387
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr
            30                  35                      40
```

```
GCG GCC CTG GCG CCG GGG GCG GCG GCC GGC AAC GAG GCG GCT CCC GCG      435
Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala
            45                  50                      55
```

```
GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG      483
Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln
            60                  65                      70
```

```
GAG CTA GCT CAG CGC GCC GCG GTG GTG ATC GAG GGA AAG GTG CAC CCG      531
Glu Leu Ala Gln Arg Ala Ala Val Val Ile Glu Gly Lys Val His Pro
            75                  80                      85
```

```
CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG      579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala
 90                  95                  100                 105
```

```
GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC      627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly
            110                 115                 120
```

```
CCA CGG GCG CTG GGG CCG CCC GCC GAG GAG CCG CTG CTC GCC GCC AAC      675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn
            125                 130                 135
```

```
GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG        723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu
    140                 145                 150

CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG        771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala
    155                 160                 165

GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG        819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu
170                 175                 180                 185

GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG        867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu
                    190                 195                 200

GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC        915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser
                    205                 210                 215

CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC        963
Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly
        220                 225                 230

CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CGG TGC GCC        1011
Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala
        235                 240                 245

TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT        1059
Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly
250                 255                 260                 265

TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC        1107
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
                    270                 175                 180

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA        1155
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys
                    185                 190                 195

CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC        1203
Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg
        200                 205                 210

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG        1251
Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
        215                 220                 225

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG        1299
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val
230                 235                 240                 245
```

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```
GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA          1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
            250             255             260

AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC          1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
            265             270             275

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC          1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            280             285             290

CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC          1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
        295             300             305

TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA                      1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
400             405             410

TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT        1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA        1650
TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT        1710
AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT        1770
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA        1830
TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA        1890
AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT        1950
CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAA AAA                2003
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 12
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: Xaa in position 11 is unknown.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
  1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 11
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: Xaa in position 9 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 12
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: Xaa in position 7 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ala Lys Glu Ala Leu Ala Ala Leu Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe Val Leu Gln Ala Lys Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
 1   5   10   15

Ile Gly Ala Tyr Thr
             20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is
                                  unknown.

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu
 1   5   10   15

Xaa Gly Xaa Gly Lys
             20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
 1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 6 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
                                  Xaa in position 11 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
                                 Xaa in position 13 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9·
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 7
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                       Xaa in position 6 is unknown.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
 1   5   10   15

Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
            20   25   30

Thr Cys Thr Cys Ala Gly Cys
            35

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 24
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
 1   5   10   15

Thr Gly Cys Cys Cys Thr Thr Cys
             20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 60
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 36
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 569
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
AAGGCGGAGG AGCTGTACCA GAAGAGAGTG CTGACCATAA CCGGCATCTG CATCGCCCTC          60
CTTGTGGTCG GCATCATGTG TGTGGTGGCC TACTGCAAAA CCAAGAAACA GCGGAAAAAG         120
CTGCATGACC GTCTTCGGCA GAGCCTTCGG TCTGAACGAA ACAATATGAT GAACATTGCC         180
AATGGGCCTC ACCATCCTAA CCCACCCCCC GAGAATGTCC AGCTGGTGAA TCAATACGTA         240
TCTAAAAACG TCATCTCCAG TGAGCATATT GTTGAGAGAG AAGCAGAGAC ATCCTTTTCC         300
ACCAGTCACT ATACTTCCAC AGCCCATCAC TCCACTACTG TCACCCAGAC TCCTAGCCAC         360
AGCTGGAGCA ACGGACACAC TGAAAGCATC CTTTCCGAAA GCCACTCTGT AATCGTGATG         420
TCATCCGTAG AAAACAGTAG GCACAGCAGC CCAACTGGGG GCCCAAGAGG ACGTCTTAAT         480
GGCACAGGAG GCCCTCGTGA ATGTAACAGC TTCCTCAGGC ATGCCAGAGA AACCCCTGAT         540
TCCTACCGAG ACTCTCCTCA TAGTGAAAG                                           569
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
Val His Gln Val Trp Ala Ala Lys
 1               5
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 10 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1               5                   10
```

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 5 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTYAARGGNG AYGCNCAYAC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATRTAYTCR TAYTCRTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGYTCNGANG CCATYTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGYTCRCTNG CCATYTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCDATNACCA TNGGNACYTT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCANA CYTGRTGNAC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCYTCNGGYT CCATRAARAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCYTCDATNA CNACRAACCA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCRAART ANCCNGC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CYTCYTTNGC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCYAANG CYTCYTTNGC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 65:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTYTTNGCYT GNAGNACRAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 20
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTYTTNGCYT GYAANACRAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 17
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGYT CYTGNAC   17

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACYAAYT CYTGNAC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATRTAYTCN CCNGARTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATRTAYTCN CCRCTRTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGARTCNGCY AANGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGARTCNGCN AGNGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

RCTRTCNGCY AANGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

RCTRTCNGCN AGNGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGARTCNGCY AARCTNGCYT T   21

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGARTCNGCN AGRCTNGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 730
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTCC ACACGCCAAG   60
CTCCCCCAAA TCGCCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT   120
GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTGACACC   180
ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCTCAG CAGTTCAGCT CCTTCCACCA   240
CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA   300
GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA   360
TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA   420
CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACAGAAGATG AAAGAGTAGG   480
TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCCTGGCA GCCAGTCTTG AGGCAACACC   540
TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCAGCAGGC CGCTTCTCGA CACAGGAAGA   600
AATCCAGGCC AGGCTGTCTA GTGTAATTGC TAACCAAGAC CCTATTGCTG TATAAAACCT   660
AAATAAACAC ATAGATTCAC CTGTAAAACT TTATTTTATA TAATAAAGTA TTCCACCTTA   720
AATTAAACAA   730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

RCTRTCNGCY AARCTNGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 21
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RCTRCTNGCN AGRCTNGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGARA TGGCTCNNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGARA TGGCAGYNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CAYCARGTNT GGGCNGCNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTYGTNGTNA THGARGGNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AARGGNGAYG CNCAYACNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GARGCNYTNG CNGCNYTNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNGGNTCNG TNCARGARYT   20

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNGGNAGYG TNCARGARYT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 21
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACYTTYTTN ARDATYTGNC C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 417
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in positions 14, 23, 90, 100, 126,
                                      and 135 is a stop codon.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA   53
      Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile
      1   5   10   15

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT   101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile
        20   25   30

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC   149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile
        35   40   45

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AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG        197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu
    50              55                  60

TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA        245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg
65              70                  75                  80

GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA        293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu
                85                  90                  95

ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG        341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu
            100                 105                 110

AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA        389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu
            115                 120                 125

ATA GAC CTG AAA TAT ATA TAG ATT ATT T                                  417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile
    130                 135
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 90:
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 33
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (ix) FEATURE:
      (D) OTHER INFORMATION: N at positions 19, 25, and 31 is Inosine.
                              Y can be cytidine or thymidine.
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGARACNC ARCCNGAYCC NGG   33

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 91:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 14, 20, 23, 29, and 35 is
                                  Inosine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGNGTRTAN GCNCCDATNA CCATNGG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 16, 21, and 24 is Inosine.
                                Y can be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCNGAYT CNGGNGARTA YATG   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 16 and 25 is Inosine. Y
                                can be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCNGAYA GYGGNGARTA YAT   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 94:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 34
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (ix) FEATURE:
              (D) OTHER INFORMATION: N at positions 14, 15, 16, 26, and 29 is
                                         Inosine. Y can be cytidine or thymidine.
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGNNNCATR TAYTCNCCNG ARTC   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 95:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 34
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (ix) FEATURE:
              (D) OTHER INFORMATION: N at positions 14, 15, 16, and 26 is
                                         Inosine. Y can be cytidine or thymidine.
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGGATCCTG CAGNNNCATR TAYTCNCCRC TRTC   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 33
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (ix) FEATURE:
              (D) OTHER INFORMATION: N at positions 21, 28, and 31 is Inosine.
                                         Y can be cytidine or thymidine.
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCAYCARG TNTGGGCNGC NAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at position 31 is Inosine. Y can be
                                      cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATHTTYT TYATGGARCC NGARG   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 18, 21, 24, 27, and 33 is
                                    Inosine. Y can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAATTCTG CAGGGGGNCC NCCNGCNTTY CCNGT   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 21 and 24 is Inosine. Y
                                    can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTYG TNGTNATHGA RGG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 17, 20, and 26 is Inosine.
                                  Y can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGCU NGCCCANACY TGRTG   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at position 19 is Inosine. Y can be
                                  cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCYTCNG GYTCCATRAA RAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 16, 22, 25, 28, and 31 is
                                  Inosine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACNGGRA ANGCNGGNGG NCC   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 35
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: N at positions 17, 26, and 29 is Inosine.
                                       Y can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGYTTNCCY TCDATNACNA CRAAC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 33
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: N at position 18 is Inosine. Y can be
                                       cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATRTAYTCR TAYTCTCNGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 33
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: N at position 19, 25, and 31 is Inosine.
                                       Y can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAARGGNG AYGCNCAYAC NGA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N at position 3 and 18 is Inosine. Y can
                                  be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCNGCYAANG CYTCYTTNGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N at position 3, 6, 9, and 18 is Inosine.
                                  Y can be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCNGCNAGNG CYTCYTTNGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N at position 3, 12, and 15 is Inosine.Y
                                  can be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCNGCRAART ANCCNGCAAG GATCCTGCAG   30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGCAGAATA TATGTGCA   38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC   37

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 117:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 39
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTCAC ACACCTGCG   39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 118:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGAA CCTGCCACAG ACTCCT   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 119:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 39
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATACCCGGGC TGCAGATGAG ATTTCACACA CCTGCGTGA   39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 120:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:
   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 16
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:
   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 13
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear
  (ix) FEATURE:
       (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:
   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23
       (B) TYPE: amino acid
       (C) STRANDEDNESS:
       (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
 1   5   10   15

Cys Gly Arg Leu Lys Glu Asp
         20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 10 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
 1   5   10   15

Ser Gly Gly Pro Gly Arg Leu
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
 1   5   10   15

Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            20   25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 129:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
 1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 130:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 23
              (B) TYPE: amino acid
              (C) STRANDEDNESS:
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
 1   5   10   15

Cys Lys Val Ile Ser Lys Leu
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 131:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 12
              (B) TYPE: amino acid
              (C) STRANDEDNESS:
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 22
              (B) TYPE: amino acid
              (C) STRANDEDNESS:
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 1   5   10   15

Lys Val Ile Ser Lys Leu
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 744
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:


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CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG   55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1                   5               10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC           103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
        20                  25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG           151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
        35                  40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC           199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50                  55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG           247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG           295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA           343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
                100                 105                 110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC           391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
                115                 120                 125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG           439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130                 135                 140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT           487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145                 150                 155                 160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC           535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                165                 170                 175
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ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT          583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile
            180                 185                 190

TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT               625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr
        195                 200                 205

TGAATCACGC AGGTGTGTGA AATCTCATTG TGAACAAATA AAAATCATGA AAGGAAAAAA      685
AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC       744




(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      134:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:     1193
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS:    single
        (D) TOPOLOGY:   linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:


CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG  55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1               5               10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC         103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20                  25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG         151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35                  40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC         199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
            50                  55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG         247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG         295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA         343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
                100                 105                 110




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TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC          391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
        115             120             125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG          439
Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
    130             135             140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT          487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145             150             155             160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC          535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
            165             170             175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA          583
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180             185             190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT          631
Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
        195             200             205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC          679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
        210             215             220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT          727
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225             230             235             240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG          775
Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu
            245             250             255

GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC            826
Val Ile Ala Ala Lys Thr Thr
            260

CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC       886
TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT       946
GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT       1006
GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT       1066
ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA       1126
GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC       1186
TCTAGAG                                                                 1193
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 1108
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:


```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG    55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1               5               10              15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC            103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
        20              25              30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG            151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
        35              40              45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC            199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50              55              60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG            247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65              70              75              80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG            295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
            85              90              95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA            343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100             105             110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC            391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115             120             125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG            439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Pro Lys
    130             135             140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT            487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145             150             155             160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC            535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                165             170             175
```

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```
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA      583
Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180                 185             190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT      631
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
            195                 200             205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC      679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            210                 215             220

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC      727
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
225                 230                 235                 240

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT      775
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
            245                 250             255

GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAGA TTCCGCCTAG  838
Glu

AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTCGCA TGAGAACATT      898
AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG      958
GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG     1018
TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA     1078
AAAAATCGAT GTCGACTCGA GATGTGGCTG                                      1108


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      136:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:   559
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS:   single
        (D) TOPOLOGY:  linear
    (ix) FEATURE:
        (D)  OTHER INFORMATION: N in position 214 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC       60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC      120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC      180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC      240
AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC      300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC      360
AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC      420
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA        474
                                            Met Ser Glu Arg Arg
                                            1                 5


150
```

```
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG          522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
              10                      15                  20

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G                        559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
              25                      30
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N in position 8 could be either A or G.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG           47
   His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser
   1            5               10                      15

CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC          95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
              20                      25                  30

TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC          143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro
              35                      40              45

GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC          191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro
              50                      55              60

CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT          239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala
              65                      70              75

GTG CAA CGG TGC G                                                        252
Val Gln Arg Cys
  80
```

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 178
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG   48
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly
 1   5   10   15

GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC   96
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
            20   25   30

TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA   144
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            35   40   45

AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G   178
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly
        50   55

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 122
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA   46
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
   1   5   10   15

GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT   94
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
            20   25   30

GCC AAC ATC ACC ATT GTG GAG TCA AAC G   122
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala
        35

152

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 417
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```
TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC    60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG        110
                         Lys Ser Glu Leu Arg Ile Ser Lys Ala
                          1               5

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA      158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
 10              15              20                      25

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT      206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly
                30              35                      40

AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC      254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile
                45              50                      55

AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG            302
Lys Val Cys Gly His Thr
                60

TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT    362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT         417
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 102
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```
AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT       47
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
 1               5               10                      15

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT      95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
                20                      25                      30

TCT TCA T                                                            102
Ser Ser Ser
        35
```

153

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 69
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:


```
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC          48
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro
 1               5                  10                  15

ATG AAA GTC CAA ACC CAA GAA                                              69
Met Lys Val Gln Thr Gln Glu
             20
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:


```
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG          48
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
 1               5                  10                  15

GCC AGC TTC TAC                                                          60
Ala Ser Phe Tyr
             20
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:


```
AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG                          36
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
 1               5                  10
```


154

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:


```
AAG CAT CTT GGG ATT GAA TTT ATG GAG                              27
Lys His Leu Gly Ile Glu Phe Met Glu
 1               5
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 569
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:


```
AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT     48
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
 1               5                  10                  15

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC     96
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
                20                  25                  30

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC    144
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
                35                  40                  45

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC    192
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
        50                  55                  60

CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA    240
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
 65                  70                  75                  80

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG    288
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
                85                  90                  95

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT    336
Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
                100                 105                 110
```

155

```
ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA        384
Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu
        115             120                 125

AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA        432
Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu
        130             135                 140

AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT        480
Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn
145             150                 155                 160

GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA        528
Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg
                165             170                 175

GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT G AAAG                 569
Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser
                180             185
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 730
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```
G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT         46
  Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp
  1               5                   10                  15

TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG        94
Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro
                20                  25                  30

CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC       142
Pro Val Ser Ser Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro
                35                  40                  45

TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG       190
Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu
            50                  55                  60

CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC TGC       238
Arg Glu Lys Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His Cys
        65                  70                  75
```

```
AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG ATA        286
Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile
 80              85                  90                  95

GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT CAA        334
Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln
                    100                 105                 110

GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA ACC        382
Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg Thr
                115                 120                 125

AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC ACA        430
Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn Thr
                130                 135                 140

GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA GTA        478
Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val
        145                 150                 155

GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC AGT        526
Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala Ser
160                 165                 170                 175

CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC CCA        574
Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn Pro
                180                 185                 190

ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC GGT        622
Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser Gly
                195                 200                 205

GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAAAACCGAA ATACACCCAT         672
Val Ile Ala Asn Gln Asp Pro Ile Ala Val
                210                 215

AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAAACAA       730


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     148:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:    1652
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS:    single
          (D) TOPOLOGY:    linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:


AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC        60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC       120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC       180
```

157

```
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA          240
GTCCCAGGTG GCCCGGACCG CACGTTGCGT CCCCGCGCTC CCCGCCGGCG ACAGGAGACG          300
CTCCCCCCCA CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA          360
AACTTTTCCC GAAGCCGATC CCAGCCCTCG GACCCAAACT TGTCGCGCGT CGCCTTCGCC          420
GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA             473
                                          Met Ser Glu Arg Arg
                                           1                 5


GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG          521
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
             10              15                  20


AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC          569
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro
             25              30                  35


CGC TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA          617
Arg Leu Lys Glu Met Lys Met Gln Glu Ser Val Ala Gly Ser Lys Leu
             40              45                  50


GTG CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG          665
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys
         55              60                  65


TGG TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC          713
Trp Phe Lys Asn Gly Ser Gly Leu Ser Arg Lys Asn Lys Pro Gln Asn
 70              75                  80                      85


ATC AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA          761
Ile Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys
                 90                  95                  100


GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA          809
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys
             105                 110                 115


CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC          857
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn
             120                 125                 130


GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT          905
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
 135                 140                 145


TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT          953
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
150                 155                 160                 165


TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG          1001
Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys
                 170                 175                 180
```

158

```
TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC          1049
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe
            185             190             195

ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA          1097
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro
            200             205             210

AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC          1145
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe
            215             220             225

TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG              1193
Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
230             235             240

CTCAGTCGGT GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT       1253
GCGTTTTACC AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG       1313
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA       1373
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC       1433
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT       1493
CGTTCCACGG GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG       1553
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT       1613
TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAAA A                           1652
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1140
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG          48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
1               5               10              15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC          96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20              25              30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG         144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35              40              45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC         192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
            50              55              60
```

159

```
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG        240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG        288
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                    85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA        336
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
                    100                 105                 110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC        384
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
                    115                 120                 125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG        432
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130                 135                 140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT        480
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145                 150                 155                 160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC        528
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                    165                 170                 175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA        576
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
                    180                 185                 190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        624
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
        195                 200                 205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        672
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
        210                 215                 220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT        720
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225                 230                 235                 240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT        768
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
                    245                 250                 255

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC        816
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
                    260                 265                 270


                              160
```

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ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG          870
Thr Pro Phe Leu Ser Leu Pro Glu
        275             280

TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT          930
GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC          990
CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG         1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG         1110
GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA                                          1140


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    150:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:    1764
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS:   single
        (D) TOPOLOGY:   linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:


G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA          49
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu
  1           5                   10                  15

TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC           97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala
            20                  25              30

AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG          145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly
        35                  40                  45

ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG          193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val
    50                  55                  60

AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA          241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
65                  70                  75                  80

TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG          289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu
                85                  90                  95

AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC          337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
            100                 105                 110

CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG          385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val
        115                 120                 125
```

161

```
GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG     433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg
    130             135             140

AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC     481
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn
145             150             155             160

ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC     529
Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro
                165             170             175

GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT     577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
            180             185             190

AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT     625
Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser
            195             200             205

CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC     673
His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro
210             215             220

AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC     721
Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Ile Ser Glu Ser
225             230             235             240

CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC     769
His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser
                245             250             255

CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT     817
Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg
            260             265             270

GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC     865
Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr
            275             280             285

CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG     913
Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg
            290             295             300

AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA     961
Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala
305             310             315             320

ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG     1009
Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys
            325             330             335
```

162

```
ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT          1057
Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala
        340                 345                 350

CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC          1105
Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro
        355                 360                 365

CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC          1153
Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro
370                 375                 380

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT          1201
Ser Met Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu
385                 390                 395                 400

GTG ACG CCA CCA CGG CTG CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA          1249
Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln
                405                 410                 415

TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC          1297
Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro
                420                 425                 430

CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG          1345
Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln
                435                 440                 445

GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC          1393
Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser
450                 455                 460

CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG          1441
Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu
465                 470                 475                 480

GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA          1489
Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu
                485                 490                 495

ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG          1537
Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln
                500                 505                 510

AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC          1585
Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val
                515                 520                 525

GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG          1633
Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu
530                 535                 540
```

163

```
CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC      1681
Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val
545             550             555             560

TAAAACCGAA ATACACCCAT AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT      1741
CCACCTTAAA TTAAACAAAA AAA                                              1764
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151:
   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 50
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
1               5               10              15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
        20              25              30

Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
        35              40              45

Phe Tyr
    50
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152:
   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 50
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
1               5               10              15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
        20              25              30

Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
        35              40              45

Val Gln
    50
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
 1   5   10   15

Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr
            20   25   30

Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser
            35   40   45

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 154:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
 1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20   25   30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC   144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
            35   40   45

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT   192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
            50   55   60

GAA TAG   198
Glu
65

165

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT   144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
                35   40   45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA   192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
    50   55   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 183
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC   144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
                35   40   45

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA   183
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr
    50   55   60

166

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 210
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC   144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
                35   40   45

GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA   192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys
        50   55   60

GCG GAG GAG CTC TAC TAA   210
Ala Glu Glu Leu Tyr
65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 267
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT   144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
                35   40   45

167

```
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT          192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
    50                  55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC          240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
65                  70                  75                  80

ACT CCC TTT CTG TCT CTG CCT GAA TAG                                       267
Thr Pro Phe Leu Ser Leu Pro Glu
                85
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT          48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1                   5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC          96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT          144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
            35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT          192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
    50                  55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG          240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu
65                  70                  75                  80

GAG CTC TAC TAA                                                          252
Glu Leu Tyr
```

168

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA          47
   Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala
    1           5               10              15

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG          95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val
             20              25              30

AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC                            128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
             35              40
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 141
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```
A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC           46
  His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser
   1           5               10              15

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC         94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser
             20              25              30

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG          141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg
             35              40              45
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in positions 15 and 22 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
 1   5   10   15

Met Val Lys Asp Leu Xaa Asn Pro
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 745
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG   48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1   5   10   15

GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG   96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
            20   25   30

CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG   144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
            35   40   45

GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG   192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
            50   55   60

TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG   240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65   70   75   80

GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA   288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
                    85   90   95

170

CTC GAC AGG AAG GCG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC   336
Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100   105   110

GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC   384
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
            115   120   125

GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC   432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
            130   135   140

ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT   480
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145   150   155   160

CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG   528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
                 165   170   175

AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC   576
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
                180   185   190

TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC   624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
            195   200   205

ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC GCC TTC CGA   672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
            210   215   220

GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC   720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225   230   235   240

AGC CGG GTG CTG TGC AAG CGG TGC G   745
Ser Arg Val Leu Cys Lys Arg Cys
            245

171

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 164:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 12
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: Xaa in position 1 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 5
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: Xaa in position 1 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Leu Val Leu Arg
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 11
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: Xaa in positions 1, 2, and 3 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn
 1   5   10

172

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 60
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: N in positions 25 and 36 is unknown.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D) OTHER INFORMATION: N in position 16 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC 18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
  1   5   10   15

Ile Gly Ala Tyr Thr
          20

173

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 422

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1               5               10              15

Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
            20              25              30

Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
        35              40              45

Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
    50              55              60

Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65              70              75              80

Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
            85              90              95

Leu Asp Arg Lys Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100             105             110

Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
        115             120             125

Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
    130             135             140

Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145             150             155             160

Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
            165             170             175

Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
            180             185             190

Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
            195             200             205

Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
210             215             220
```

174

```
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225                 230             235             240

Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu
                245                 250             255

Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys
                260                 265             270

Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn
        275             280             285

Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln
    290             295                 300

Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
305             310                 315                 320

Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp
                325                 330                 335

Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr
            340                 345             350

Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys
        355             360                 365

Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser
    370             375             380

Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp
385             390                 395             400

Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
            405             410             415

Phe Leu Ser Leu Pro Glu
        420
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1               5               10              15
```

175

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
                  20   25   30

Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
          35   40   45

Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
      50   55   60

Asn Thr Ser Ser Ser
65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1   5   10   15

Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 231
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAGCGCC TCAGCGCGGC CGCTCGCTCT CCCCCTCGAG GGACAAACTT TTCCCAAACC   60
CGATCCGAGC CCTTGGACCA AACTCGCCTG CGCCGAGAGC CGTCCGCGTA GAGCGCTCCG   120
TCTCCGGCGA GATGTCCGAG CGCAAAGAAG GCAGAGGCAA AGGGAAGGGC AAGAAGAAGG   180
AGCGAGGCTC CGGCAAGAAG CCGGAGTCCG CGGCGGGCAG CCAGAGCCCA G   231

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC CCGATTGAAA GAGATGAAAA GCCAGGAATC GGCTGCAGGT TCCAAACTAG   60
TCCTTCGGTG TGAAACCAGT TCTGAATACT CCTCTCTCAG ATTCAAGTGG TTCAAGAATG   120
GGAATGAATT GAATCGAAAA AACAAACCAC AAAATATCAA GATACAAAAA AAGCCAGG   178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 122
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA CTTCGCATTA ACAAAGCATC ACTGGCTGAT TCTGGAGAGT ATATGTGCAA   60
AGTGATCAGC AAATTAGGAA ATGACAGTGC CTCTGCCAAT ATCACCATCG TGGAATCAAA   120
CG   122

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 176:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 102
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC TGGTATGCCA GCCTCAACTG AAGGAGCATA TGTGTCTTCA GAGTCTCCCA   60
TTAGAATATC AGTATCCACA GAAGGAGCAA ATACTTCTTC AT   102

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 177:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAA ATGTGCGGAG AAGGAGAAAA   60
CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT   120
ACTTGTGC   128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 178:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA   60
AACCAAGAA   69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 179:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA   23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT   23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 22
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCCTCCTT GA   22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 22
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA   22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GGCGGCGAAA   20